



# UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/086,748	02/28/2002	Paul K. Wolber	10020405-1	8764

7590 01/06/2006  
AGILENT TECHNOLOGIES, INC.  
Legal Department, DL429  
Intellectual Property Administration  
P.O. Box 7599  
Loveland, CO 80537-0599

EXAMINER

ZHOU, SHUBO

ART UNIT PAPER NUMBER

1631

DATE MAILED: 01/06/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

# Office Action Summary

Application No.

10/086,748

Applicant(s)

WOLBER ET AL.

Examiner

Shubo (Joe) Zhou

Art Unit

1631

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

## Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

## Status

- 1) ☒ Responsive to communication(s) filed on 9/2/05 and 11/7/05.
- 2a) ☐ This action is **FINAL**. 2b) ☒ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

## Disposition of Claims

- 4) ☒ Claim(s) 1-8, 10-12, 15 and 16 is/are pending in the application.
- 4a) Of the above claim(s) 16 is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-8, 10-12 and 15 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

## Application Papers

- 9) ☒ The specification is objected to by the Examiner.
- 10) ☒ The drawing(s) filed on 11 June 2002 is/are: a) ☒ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

## Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).
- \* See the attached detailed Office action for a list of the certified copies not received.

## Attachment(s)

- 1) ☐ Notice of References Cited (PTO-892)
- 2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
- 3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08)  
Paper No(s)/Mail Date \_\_\_\_\_.
- 4) ☐ Interview Summary (PTO-413)  
Paper No(s)/Mail Date. \_\_\_\_\_.
- 5) ☐ Notice of Informal Patent Application (PTO-152)
- 6) ☐ Other: \_\_\_\_\_.

## DETAILED ACTION

### *Request for Continued Examination*

1. A request for continued examination under 37 CFR 1.114, including the fee set forth in 37 CFR 1.17(e), was filed in this application after final rejection. Since this application is eligible for continued examination under 37 CFR 1.114, and the fee set forth in 37 CFR 1.17(e) has been timely paid, the finality of the previous Office action has been withdrawn pursuant to 37 CFR 1.114. Applicant's submission filed on 9/2/05 has been entered.

Claims 1-8, 10-12, and 15-16 are currently pending with 15-16 newly added.

2. Newly submitted claim 16 is directed to an invention that is independent or distinct from the invention originally claimed for the following reasons:

Claim 16 is directed to a method that comprises distinct steps from the claims under consideration. It comprises determining a mole fraction of samples that hybridize to the calibrating features and calculating normalized intensities based thereupon.

Since applicant has received an action on the merits for the originally presented invention, this invention has been constructively elected by original presentation for prosecution on the merits. Accordingly, claim 16 is withdrawn from consideration as being directed to a non-elected invention. See 37 CFR 1.142(b) and MPEP § 821.03.

***Specification***

3. The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. While the amendment filed 11/5/04 deleted some of the codes, such embedded hyperlinks are still present in the specification, such on page 35, line 8.

***Claim Rejections-35 USC § 112***

4. The following is a quotation of the first paragraph of 35 U.S.C. 112:

The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

5. Claim 10 is rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

Claim 10 is amended to recite “each normalized signal intensity being functionally related to a mole fraction of sample molecules that hybridize to the respective feature.” There is no adequate description of this limitation in the specification. While the specification describes calculation of a mole fraction (see pages 23-24), it does not provide description of “each normalized signal intensity being functionally related to a mole fraction of sample molecules that hybridize to the respective feature.” This amended claim thus contains new matter.

6. The following is a quotation of the **second** paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

7. Claim 10 is rejected under 35 U.S.C. 112 , second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 10 is amended to recite “each normalized signal intensity being functionally related to a mole fraction of sample molecules that hybridize to the respective feature.” The metes and bounds of the limitation are unclear because the meaning of the phrase “functionally related” is vague in the context of the claim. It is not clear what is meant by having a signal intensity functionally related to a fraction of molecules in a sample. It is not clear how the signal intensity, which reflects the level of molecules in the sample, can relate to the function of the molecules.

***Claim Rejections-35 USC § 102***

8. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

9. Claims 1, 7-8, and 15 are rejected under 35 U.S.C. 102(b) as being anticipated by Lockhart et al. (IDS document: WO 97/10365, 3/20/1997).

The claims are drawn to a method of calibrating molecular array data comprising using a molecular array containing calibrating probes that hybridize to a sufficient fraction of target molecules in a sample to produce a signal intensity, and normalizing signals of features on the array using the calibrating probes by calculating a collective signal intensity. Due to lack of a specific definition for the term “collective signal intensity” in the specification, it is interpreted as total signal intensities of the calibrating probes (collective: assembled or accumulated into a whole. Dictionary.com <http://dictionary.reference.com/search?q=collective>).

Lockhart et al. disclose a method of using oligonucleotide array for monitoring gene expression. The method comprises using an array containing not only oligonucleotide probes referred to as “test probes”, but also control probes used for calibration. The control probes include normalization controls, expression level controls such as probes from housekeeping genes, and mismatch controls. In one embodiment, Lockhart et al. teach that the difference between signal intensities of a perfect match (PM) probe and a mismatch (MM) probe for each pair of PM and MM are calculated, and then the average of the differences for all the pairs is calculated. See page 61, first paragraph and page 103, claims 66-67. It would be readily recognized by one of skill in the art that when the average difference is calculated, a total intensity of the difference between the PM and MM must have also been calculated. Consequently, the total intensities of all MM probes are also calculated. All the control probes disclosed by Lockhart et al. are interpreted as calibrating probes as in the instant claims because they are used to calibrate the signals of the test probes. The calibrating probes disclosed by Lockhart et al. will hybridize to a fraction of the target molecules in the sample solutions to which the array is exposed for hybridization because the products of the housekeeping genes, etc.

Art Unit: 1631

are contained in the sample solutions. Further, since MM probes for each target is included as a control probes, which will hybridize to its target under certain stringencies albeit maybe nonspecifically. Since the specification does not explicitly define the term “sufficient fraction of target molecules”, it is broadly interpreted as any fraction that is sufficient to generate a signal by either specific or nonspecific hybridizations. As to the limitation that producing signal intensities upon reading of calibrating probes proportional to the total concentration of target molecules in the sample, it would be readily recognized by one of skill in the art that it is an inherent principle of using microarray for assessing gene expression that the signals produced by hybridization of probes on the array with the target molecules in the sample are indicative of the levels of target molecules in the sample, i.e. signal being proportional to the concentration of target molecules in the sample. As to the new limitation amended into claim 1, “a set of features containing probes that hybridize to specific target molecules under stringent conditions,” the specific probes, i.e. the “test probes” on the array of Lockhart et al., are probes that would hybridize to specific target molecules in a sample under stringent conditions.

In regard to claims 7-8, which require that a set of similar calibrating signal intensities that each covers a discrete range of signal intensities generated from the features of the array, Lockhart et al. teach that each PM signal intensity is calibrated by calculating the difference between signal intensities of the PM and its corresponding MM. The signal intensity for every PM probe is similarly calibrated. The average difference for all PM/MM is also calculated. Each signal can then be calibrated thereupon. Each of these PM-MM signal intensities is interpreted as a calibrating signal intensity. Since all the differences of PM-MM are calculated similarly, they are interpreted as similar calibrating signal intensities. Because these differences of PM-

MM as a whole represent the signal intensities for all the probes on the array, they cover the entire span, i.e. overall range of signal intensities generated from the array.

Applicants' arguments filed 9/2/05 has been fully considered but they are not deemed persuasive. Applicants argue that Lockhart et al. do not calculate the total intensity of all the PM and MM probes, but rather only those that incremented NPOS or NNEG. This is not persuasive because claim 1 recites calculating a collective signal intensity from the signal intensities read from the entire set of calibrating features, and in Lockhart et al., the set of probes that incremented NPOS or NNEG is the set of calibrating probes because their intensities are factored in the calibration. And it is the total intensities of these probes that are calculated.

***Claim Rejections-35 USC § 103***

10. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

The factual inquiries set forth in *Graham v. John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

11. Claims 2-3, 5, and 10-12 are rejected under 35 U.S.C. 103(a) as being unpatentable over Lockhart et al. (WO 97/10365, 3/20/1997), as applied to claims 1, 7-8 and 15 above, in view of Chenchik et al. (US patent no. 6,077,673, Date of Patent: June 20, 2000) and further in view of Lewin, B., (Genes IV, 1990, Oxford University Press).

The instant claims are drawn to a method of calibrating molecular array data comprising using a molecular array containing calibrating probes that either hybridize to a sufficient fraction of target molecules in a sample solution to which the array is exposed for hybridization, as is in claims 2-3 and 5, or hybridize to a majority of target molecules in the sample solution, as is in claims 10-12, and normalizing signals of features on the array using the calibrating probes by calculating a collective signal intensity. Claims 2-3 recite that the calibrating probes are poly(A) oligonucleotides, and claim 5 recites that the calibrating probes are oligonucleotides complementary to a synthetic nucleotide sequence appended to primers for reverse transcription of the mRNA molecules.

As applied to claims 1, 7-8, and 15 above, Lockhart et al. disclose a method of using oligonucleotide array for monitoring gene expression. The method comprises using an array

Art Unit: 1631

containing not only oligonucleotide probes referred to as “test probes”, but also control probes used for calibration. The control probes include normalization controls, expression level controls such as probes from housekeeping genes, and mismatch controls. In one embodiment, Lockhart et al. teach that the difference between signal intensities of a perfect match (PM) probe and a mismatch (MM) probe for each pair of PM and MM are calculated, and then the average of the differences for all the pairs is calculated. See page 61, first paragraph and page 103, claims 66-67. It would be readily recognized by one of skill in the art that when the average difference is calculated, a total intensity of the difference between the PM and MM must have also been calculated. Consequently, the total intensities of all MM probes are also calculated. All the control probes disclosed by Lockhart et al. are interpreted as calibrating probes as in the instant claims because they are used to calibrate the signals of the test probes. The calibrating probes disclosed by Lockhart et al. will hybridize to a fraction of the target molecules in the sample solutions to which the array is exposed for hybridization because the products of the housekeeping genes, etc. are contained in the sample solutions. Further, since MM probes for each target is included as a control probes, which will hybridize to its target under certain stringencies albeit maybe nonspecifically. Since the specification does not explicitly define the term “sufficient fraction of target molecules”, it is broadly interpreted as any fraction that is sufficient to generate a signal by either specific or nonspecific hybridizations.

Lockhart et al. do not explicitly teach (1) that poly(A) oligonucleotides are used as calibrating probes; (2) that the calibrating probes are oligonucleotides complementary to a synthetic nucleotide sequence appended to primers for reverse transcription of the mRNA

molecules; and (3) that the calibrating probes hybridize to a majority of the target molecules in the sample solution to which the array is exposed.

Chenchik et al. disclose a nucleic acid microarray and a process of using same for gene expression monitoring. The array is exposed to a sample solution containing cDNA molecules derived from the mRNA from a biological sample. In addition to the “probe spots”, the array also comprises “calibration spots” and “control spots” (column 4, lines 12-20). Chenchik et al. indicate that the calibrating and control spots are to “provide other useful information, such as background or basal level of expression, and the like”, and such spots “serve in the normalization of mRNA abundance and standardization of hybridization signal intensity in the sample assayed with the array” (column 8, lines 50-67 and column 9). While Chenchik et al. do not explicitly disclose using poly(A) oligonucleotides as calibrating spots, they do motivate/suggest doing such by emphasizing that the calibrating probes should not be unique to a particular target in the sample, but “common” to the targets (column 8, lines 50-67).

Lewin teaches that poly(A) tail is common to eukaryotic, such as human mRNA. See pages 178-179.

Since the target molecules contained in the sample solutions to which the array is exposed for hybridization in the method disclosed by Lockhart et al. are cDNAs, and since the cDNAs are derived from mRNAs by reverse transcription using oligo(dT) as primers followed by PCR amplification (Lockhart et al. page 39), it would have been obvious to one of ordinary skill in the art that oligo(dT) or poly(A) would be commonly present in the cDNA targets due to the way they are made, and one of ordinary skill in the art would have been motivated by Chenchik et al. to modify the method of Lockhart et al. to use calibrating probes that are common to the target molecules, and would have been motivated by Lewin to include poly(A) oligonucleotides on the array as extra calibrating probes. Such poly(A) oligonucleotides would hybridize to the majority of the target molecules because of the presence of oligo(dT) therein.

Further, such poly(A) oligonucleotides calibrating probes would be complementary to the oligo(dT) portion of the target molecules, which oligo(dT) is a synthetic nucleotide sequence that is appended to primers for reverse transcription of the mRNA molecules during the process of preparing target molecules for hybridization. This thus reads on the specific requirement by claim 5.

There would have been a reasonable expectation of success because Lockhart et al. and Chenchik et al. provide the details of procedures for making an array, preparing cDNA samples for hybridization, and making poly(A) oligonucleotides would have been known and routine skill in the art. Note that by poly(A) oligonucleotides it is meant that the oligonucleotides consist of, or comprise, consecutive multiple “As”.

Applicants’ arguments filed 9/2/05 have been fully considered but they are not deemed persuasive. Applicants argue again that Lockhart et al. do not calculate the total intensity of all the PM and MM probes, but rather only those that incremented NPOS or NNEG. This is not persuasive because the claims, such as claim 1, recites calculating a collective signal intensity from the signal intensities read from the entire set of calibrating features, and in Lockhart et al., the set of probes that incremented NPOS or NNEG is the set of calibrating probes because their intensities are factored in the calibration. And it is the total intensities of these probes that are calculated. Applicants also argue that Lockhart et al. do not calculate normalized signal intensities for features that are not in the set of control features.” This is not persuasive because this limitation is not recited in the claims. Applicants further argue that Chenchik et al. do not teach or suggest a normalization procedure based on calibration probes, etc. This is found persuasive because Chenchik et al. do indeed disclose using “calibration spots” and “control spots” on their array (column 4, lines 12-20), indicate that the calibrating and control spots are to “provide other useful information, such as background or basal level of expression, and the like”, and state that such spots “serve in the normalization of mRNA abundance and standardization of

hybridization signal intensity in the sample assayed with the array” (column 8, lines 50-67 and column 9). Further, it is noted that the significance of the teaching of Chenchik et al. is that they motivate/suggest using calibrating probes that should not be unique to a particular target in the sample, but “common” to the targets (column 8, lines 50-67).

12. Claim 4 is rejected under 35 U.S.C. 103(a) as being unpatentable over Lockhart et al. (WO 97/10365, 3/20/1997), as applied to claims 1, 7-8, and 15 above, in view of Chenchik et al. (US patent no. 6,077,673, Date of Patent: June 20, 2000) and further in view of Darnell et al. (Molecular Cell Biology, Eds., 1990, published by Scientific American Books).

The instant claims are drawn to a method of calibrating molecular array data comprising using a molecular array containing calibrating probes that either hybridize to a sufficient fraction of target molecules in a sample solution to which the array is exposed for hybridization or hybridize to a majority of target molecules in the sample solution, and normalizing signals of features on the array using the calibrating probes by calculating a collective signal intensity. Claim 4 also requires that the calibrating probes comprise Alu repeat sequences.

As applied to claims 1, 7-8, and 15 above, Lockhart et al. disclose a method of using oligonucleotide array for monitoring gene expression. The method comprises using an array containing not only oligonucleotide probes referred to as “test probes”, but also control probes used for calibration. The control probes include normalization controls, expression level controls such as probes from housekeeping genes, and mismatch controls. In one embodiment, Lockhart et al. teach that the difference between signal intensities of a perfect match (PM) probe and a mismatch (MM) probe for each pair of PM and MM are calculated, and then the average of the differences for all the pairs is calculated. See page 61, first paragraph and page 103, claims 66-

67. It would be readily recognized by one of skill in the art that when the average difference is calculated, a total intensity of the difference between the PM and MM must have also been calculated. Consequently, the total intensities of all MM probes are also calculated. All the control probes disclosed by Lockhart et al. are interpreted as calibrating probes as in the instant claims because they are used to calibrate the signals of the test probes. The calibrating probes disclosed by Lockhart et al. will hybridize to a fraction of the target molecules in the sample solutions to which the array is exposed for hybridization because the products of the housekeeping genes, etc. are contained in the sample solutions. Further, since MM probes for each target is included as a control probes, which will hybridize to its target under certain stringencies albeit maybe nonspecifically. Since the specification does not explicitly define the term “sufficient fraction of target molecules”, it is broadly interpreted as any fraction that is sufficient to generate a signal by either specific or nonspecific hybridizations.

Lockhart et al. do not explicitly recite that oligonucleotide comprising Alu sequences are used as calibrating probes.

Chenchik et al. disclose a nucleic acid microarray and a process of using same for gene expression monitoring. The array is exposed to a sample solution containing cDNA molecules derived from the mRNA from a biological sample. In addition to the “probe spots”, the array also comprises “calibration spots” and “control spots” (column 4, lines 12-20). Chenchik et al. indicate that the calibrating and control spots are to “provide other useful information, such as background or basal level of expression, and the like”, and such spots “serve in the normalization of mRNA abundance and standardization of hybridization signal intensity in the sample assayed with the array” (column 8, lines 50-67 and column 9). While Chenchik et al. do not explicitly disclose using poly(A) oligonucleotides as calibrating spots, they do motivate/suggest doing such

by emphasizing that the calibrating probes should not be unique to a particular target in the sample, but “common” to the targets (column 8, lines 50-67).

Darnell et al. teach that Alu sequence is common to human genes and mRNA (see pages 373-374).

A person of ordinary skill in the art would have been motivated by Chenchik et al. to include calibrating probes that are common to the targets in the sample solution to modify Lockhart et al. to provide more calibrating probes for the microarray analysis.

The teaching of Darnell et al. makes it obvious to one of ordinary skill in the art that such common Alu sequence would meet the requirement for a calibrating probe set by Chenchik et al. Thus, one of ordinary skill in the art would have been motivated by Chenchik et al. and Darnell et al. to modify the method of Lockhart et al. to include oligonucleotides comprising Alu sequences on the array as extra calibrating probes. There would have been a reasonable expectation of success because Lockhart et al. and Chenchik et al. provide the details of procedures for making an array, preparing cDNA samples for hybridization, and making oligonucleotides comprising Alu sequence would have been known and routine skill in the art.

Applicants’ arguments filed 9/2/05 have been fully considered but they are not deemed persuasive. The arguments are toward Lockhart et al. and Chenchik et al., and the arguments are the same as those provided for the rejection of paragraph 11. The arguments are not found persuasive for reasons set forth above in those respective sections.

13. Claim 6 is rejected under 35 U.S.C. 103(a) as being unpatentable over Lockhart et al. (WO 97/10365, 3/20/1997), as applied to claims 1, 7-8, and 15 above, in view of Chenchik et al. (US patent no. 6,077,673, Date of Patent: June 20, 2000) and further in view of Feinberg et al. (Analytical Biochemistry, Vol. 132, pages 6-13, 1983).

The instant claims are drawn to a method of calibrating molecular array data comprising using a molecular array containing calibrating probes that either hybridize to a sufficient fraction of target molecules in a sample solution to which the array is exposed for hybridization, and normalizing signals of features on the array using the calibrating probes by calculating a collective signal intensity. Claim 6 also requires that the calibrating probes are random sequence oligonucleotide.

As applied to claims 1, 7-8, and 15 above, Lockhart et al. disclose a method of using oligonucleotide array for monitoring gene expression. The method comprises using an array containing not only oligonucleotide probes referred to as “test probes”, but also control probes used for calibration. The control probes include normalization controls, expression level controls such as probes from housekeeping genes, and mismatch controls. In one embodiment, Lockhart et al. teach that the difference between signal intensities of a perfect match (PM) probe and a mismatch (MM) probe for each pair of PM and MM are calculated, and then the average of the differences for all the pairs is calculated. See page 61, first paragraph and page 103, claims 66-67. It would be readily recognized by one of skill in the art that when the average difference is calculated, a total intensity of the difference between the PM and MM must have also been calculated. Consequently, the total intensities of all MM probes are also calculated. All the control probes disclosed by Lockhart et al. are interpreted as calibrating probes as in the instant claims because they are used to calibrate the signals of the test probes. The calibrating probes disclosed by Lockhart et al. will hybridize to a fraction of the target molecules in the sample solutions to which the array is exposed for hybridization because the products of the housekeeping genes, etc. are contained in the sample solutions. Further, since MM probes for

Art Unit: 1631

each target is included as a control probes, which will hybridize to its target under certain stringencies albeit maybe nonspecifically. Since the specification does not explicitly define the term “sufficient fraction of target molecules”, it is broadly interpreted as any fraction that is sufficient to generate a signal by either specific or nonspecific hybridizations.

Lockhart et al. do not explicitly recite that random sequence oligonucleotide are used as calibrating probes.

Chenchik et al. disclose a nucleic acid microarray and a process of using same for gene expression monitoring. The array is exposed to a sample solution containing cDNA molecules derived from the mRNA from a biological sample. In addition to the “probe spots”, the array also comprises “calibration spots” and “control spots” (column 4, lines 12-20). Chenchik et al. indicate that the calibrating and control spots are to “provide other useful information, such as background or basal level of expression, and the like”, and such spots “serve in the normalization of mRNA abundance and standardization of hybridization signal intensity in the sample assayed with the array” (column 8, lines 50-67 and column 9). While Chenchik et al. do not explicitly disclose using poly(A) oligonucleotides as calibrating spots, they do motivate/suggest doing such by emphasizing that the calibrating probes should not be unique to a particular target in the sample, but “common” to the targets (column 8, lines 50-67).

Feinberg et al. teach a method of labeling a DNA by using a mixture of random hexamer as primers and state that the oligonucleotides bind to any DNA in high frequency. see page 6, abstract and pages 7-11).

A person of ordinary skill in the art would have been motivated by Chenchik et al. to include calibrating probes that are common to the targets in the sample solution to modify Lockhart et al. to provide more calibrating probes for the microarray analysis.

The teaching of Feinberg et al. makes it obvious to one of ordinary skill in the art that the random hexamer oligonucleotides would be ideal for a calibrating probe because it would meet the “common” standard proposed by Chenchik et al. Thus, one of ordinary skill in the art would have been motivated by Chenchik et al. and Feinberg et al. to modify the method of Lockhart et al. to include random hexamer oligonucleotides on the array as extra calibrating probes. There would have been a reasonable expectation of success because Lockhart et al. and Chenchik et al. provide the details of procedures for making an array, preparing cDNA samples for hybridization, and making random hexamer oligonucleotides would have been known and routine skill in the art, and the random primers would have been actually commercially available.

Applicants’ arguments filed 9/2/05 have been fully considered but they are not deemed persuasive. Applicants do not argue specifically against this rejection, but rather assert that newly added claims 15 and 16 would be allowable. This is not persuasive because new claim 15 is rejected for reasons set forth in paragraph 9, and claim 16 is withdrawn from further consideration as being drawn to non-elected invention.

### ***Conclusion***

14. No claim is allowed.

15. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Shubo (Joe) Zhou, whose telephone number is 571-272-0724.

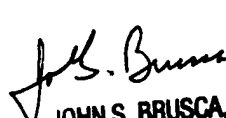
The examiner can normally be reached Monday-Friday from 8 A.M. to 4 P.M. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Ardin Marschel, Ph.D., can be reached on 571-272-0718. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to Patent Analyst Tina Plunkett whose phone number is (571) 272-0549.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public. For all other customer support, please call the USPTO Call Center (UCC) at 800-786-9199.

Shubo (Joe) Zhou, Ph.D.



Patent Examiner

 3 January 2006  
JOHN S. BRUSCA, PH.D.  
PRIMARY EXAMINER